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TITLE: Identifying optimal primers for amplification, useful e.g. in medicine,
to generate many overlapping or adjacent fragments

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PATENT-FAMILY:

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ABSTRACTED-PUB-NO: DE 10062566A

BASIC-ABSTRACT: NOVELTY - Identifying primer sequences, and pairs, for
generating many adjacent or overlapping PCR (polymerase chain reaction)
fragments from a given DNA sequence (I), is new.

DETAILED DESCRIPTION - Identifying primer sequences, and pairs, for generating
many adjacent or overlapping PCR (polymerase chain reaction) fragments from a
given DNA sequence (I), is new. A list is first drawn up of fragments (II) of
(I) that, from their length, are potential primers. The values of
characteristic parameters (CP) for each (II) are determined, with at least one
CP being evaluated continuously. Value ranges for CP are determined and from
these parameters (II) are classified as optimal or unsuitable for use as
primers. The value ranges are separated by a transition region that can be
represented by a transition function, continuous and with a strongly monotonic
progression. Each CP value in this region is assigned a rating corresponding
to the size of the appropriate transition function. (II) that are unsuitable,
on the basis of one or more CP, are discarded and the other (II) are given a
combined score (CS) by weighted summation of the sizes evaluated above and
those having CS that meet predetermined criteria are selected. The selected
sequences are then stored, displayed and/or output as primers and arranged into
pairs.

INDEPENDENT CLAIMS are also included for the following:

(1) computer program for the novel process; and

(2) device for performing the novel process.

USE - The method is used to design primers for PCR, e.g. for use in biology, biotechnology, human or veterinary medicine, agriculture etc.

ADVANTAGE - The method allows automated discovery of optimal primer pairs. It provides a more objective and realistic evaluation than known methods and makes possible rational analysis of long DNA fragments in the form of overlapping sequences, with high analytical throughput, lower dropout rates and savings in materials, labor and time.